

# Sequence Listing

<110> de Sauvage, Frederic J.  
Gurney, Austin  
Murone, Maximilien  
Rosenthal, Arnon  
Stone, Donna M.  
Wood, William I.



<120> Human Suppressor of Fused

<130> P1548R1-US

<150> US 60/123,090

<151> 1999-03-05

<150> US 60/135,736

<151> 1999-05-25

<150> PCT/US00/05746

<151> 2000-03-02

<160> 10

<210> 1

<211> 1760

<212> DNA

<213> Homo sapiens

<400> 1

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cgcttcgctc tttcccccg gactgcacgc catctacgga gagtgccgcc 200
gcctttaccc tgaccagccg aaccgcctcc aggttacccg tatcgtcaag 250
tactggttgg gtggcccaga ccccttggac tatgttagca tgtacaggaa 300
tgtgggggagc cttctgcta acatccccga gcaactggac tacatcagct 350
tcggcctgag tgatctctat ggtgacaaca gagtccatga gtttacagga 400
acagatggac ctagtggttt tggctttgag ttgacctttc gtctgaagag 450
agaaactggg gagtctgccc caccaacatg gcccgagag ttaatgcagg 500
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catgctgctg acagaggacc cacagatgca gcccgtcag acacctttg 650
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gcctattgct ggcgggccct ggctgataac tgacatgcgg aggggagaga 800

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ccatatttga gatcgatcca cacctgcaag agagagttga caaaggcatc 850  
gagacagatg gctccaacct gagtggtgtc agtgccaagt gtgcctggga 900  
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tcggcacaca gccccggcga ctctctggca aagacacaga gcagatccgg 1000  
gagaccctga ggagaggact cgagatcaac agcaaacctg tccttccacc 1050  
aatcaaccct cagcggcaga atggcctcgc ccacgaccgg gccccgagcc 1100  
gcaaagacag cctggaaagt gacagctcca cggccatcat tccccatgag 1150  
ctgattcgca cgcggcagct tgagagcgta catctgaaat tcaaccagga 1200  
gtccggagcc ctcatctc tctgcctaag gggcaggctc ctgcatggac 1250  
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<211> 431  
<212> PRT  
<213> Homo sapiens

<400> 2  
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Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr  
35 40 45  
Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr  
50 55 60  
Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg  
65 70 75

Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr  
 80 85 90  
 Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His  
 95 100 105  
 Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
 110 115 120  
 Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr  
 125 130 135  
 Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln  
 140 145 150  
 Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser  
 155 160 165  
 Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr  
 170 175 180  
 Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val  
 185 190 195  
 Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser  
 200 205 210  
 Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr  
 215 220 225  
 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg  
 230 235 240  
 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val  
 245 250 255  
 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser  
 260 265 270  
 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp  
 275 280 285  
 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu  
 290 295 300  
 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly  
 305 310 315  
 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln  
 320 325 330  
 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp  
 335 340 345  
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu  
 350 355 360  
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln  
 365 370 375

Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu  
380 385 390

His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala  
395 400 405

Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu  
410 415 420

Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu  
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<210> 3  
<211> 346  
<212> DNA  
<213> Artificial sequence

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<223> consensus DNA used to isolate DNA 33454

<220>  
<221> unsure  
<222> 8, 28, 39, 54-55, 65, 68, 74, 80, 90, 125, 130  
<223> unknown base

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gccatctacg gagagtgccg ccgntttan ccttaccagc cgaacccgct 150  
ccagggttacc gctatcgtca agtactgggt ggggtggcca gaccccttgg 200  
actatggttag catgtacagg aatgtgggga gcccttctgc taacatcccc 250  
gagcactggc actacatcag cttcggcctg agtgatctct atggtgacaa 300  
cagagtccat gaagtttaca ggaacagatg gacctagtgg ttttgt 346

<210> 4  
<211> 468  
<212> PRT  
<213> Drosophila Melanogaster

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Asn Gln Pro Asn Pro Leu Gln Val Thr Thr Leu Leu Lys Tyr Trp  
35 40 45  
Leu Gly Gly Gln Asp Pro Leu Asp Tyr Ile Ser Met Tyr Lys Phe  
50 55 60  
Pro Gly Asp Val Asp Arg Asn Val Pro Pro His Trp His Tyr Ile  
65 70 75

Ser Phe Gly Leu Ser Asp Leu His Gly Asp Glu Arg Val His Leu  
 80 85 90  
 Arg Glu Glu Gly Val Thr Arg Ser Gly Met Gly Phe Glu Leu Thr  
 95 100 105  
 Phe Arg Leu Ala Lys Thr Glu Ile Glu Leu Lys Gln Gln Ile Glu  
 110 115 120  
 Asn Pro Glu Lys Pro Gln Arg Ala Pro Thr Trp Pro Ala Asn Leu  
 125 130 135  
 Leu Gln Ala Ile Gly Arg Tyr Cys Phe Gln Thr Gly Asn Gly Leu  
 140 145 150  
 Cys Phe Gly Asp Asn Ile Pro Trp Arg Lys Ser Leu Asp Gly Ser  
 155 160 165  
 Thr Thr Ser Lys Leu Gln Asn Leu Leu Val Ala Gln Asp Pro Gln  
 170 175 180  
 Leu Gly Cys Ile Asp Thr Pro Thr Gly Thr Val Asp Phe Cys Gln  
 185 190 195  
 Ile Val Gly Val Phe Asp Asp Glu Leu Glu Gln Ala Ser Arg Trp  
 200 205 210  
 Asn Gly Arg Gly Val Leu Asn Phe Leu Arg Gln Asp Met Gln Thr  
 215 220 225  
 Gly Gly Asp Trp Leu Val Thr Asn Met Asp Arg Gln Met Ser Val  
 230 235 240  
 Phe Glu Leu Phe Pro Glu Thr Leu Leu Asn Leu Gln Asp Asp Leu  
 245 250 255  
 Glu Lys Gln Gly Ser Asp Leu Ala Gly Val Asn Ala Asp Phe Ser  
 260 265 270  
 Phe Arg Glu Leu Lys Pro Thr Lys Glu Val Lys Glu Glu Val Asp  
 275 280 285  
 Phe Gln Ala Leu Ser Glu Lys Cys Ala Asn Asp Glu Asn Asn Arg  
 290 295 300  
 Gln Leu Thr Asp Thr Gln Met Lys Arg Glu Glu Pro Ser Phe Pro  
 305 310 315  
 Gln Ser Met Ser Met Ser Ser Asn Ser Leu His Lys Ser Cys Pro  
 320 325 330  
 Leu Asp Phe Gln Ala Gln Ala Pro Asn Cys Ile Ser Leu Asp Gly  
 335 340 345  
 Ile Glu Ile Thr Leu Ala Pro Gly Val Ala Lys Tyr Leu Leu Leu  
 350 355 360  
 Ala Ile Lys Asp Arg Ile Arg His Gly Arg His Phe Thr Phe Lys  
 365 370 375  
 Ala Gln His Leu Ala Leu Thr Leu Val Ala Glu Ser Val Thr Gly

	380		385		390
Ser Ala Val Thr	Val Asn Glu Pro Tyr	Gly Val Leu Gly Tyr Trp			
	395	400		405	
Ile Gln Val Leu	Ile Pro Asp Glu Leu	Val Pro Arg Leu Met Glu			
	410	415		420	
Asp Phe Cys Ser	Ala Gly Leu Asp Glu	Lys Cys Glu Pro Lys Glu			
	425	430		435	
Arg Leu Glu Leu	Glu Trp Pro Asp Lys	Asn Leu Lys Leu Ile Ile			
	440	445		450	
Asp Gln Pro Glu	Pro Val Leu Pro Met	Ser Leu Asp Ala Ala Pro			
	455	460		465	
Leu Lys Met					

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 <211> 275  
 <212> DNA  
 <213> Mus musculus

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 catgtacagg aacatgggga gtccttctgc caacatccct gagcactggc 150  
 actacatcag ctttggcctg agtgatctct atgggtgacaa cagagtccat 200  
 gagtttacag gaacagacgg accaagtgga tttggctttg agttgacgtt 250  
 tcgtctgaag agagaaactg gggag 275

<210> 6  
 <211> 23  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> forward PCR cloning primer

<400> 6  
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<210> 7  
 <211> 25  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> reverse PCR cloning primer

<400> 7  
 catggactct gttgtcacca tagag 25

<210> 8

<211> 40  
<212> DNA  
<213> Artificial sequence

<220>  
<223> hybridization probe

<400> 8  
gagcactggc actacatcag ctttggcctg agtgatctct 40

<210> 9  
<211> 441  
<212> PRT  
<213> Artificial sequence

<220>  
<223> hSu(fu) epitope flag protein

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Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr  
35 40 45  
Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr  
50 55 60  
Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg  
65 70 75  
Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr  
80 85 90  
Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His  
95 100 105  
Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
110 115 120  
Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr  
125 130 135  
Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln  
140 145 150  
Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser  
155 160 165  
Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr  
170 175 180  
Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val  
185 190 195  
Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser  
200 205 210

Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr  
 215 220 225  
 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg  
 230 235 240  
 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val  
 245 250 255  
 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser  
 260 265 270  
 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp  
 275 280 285  
 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu  
 290 295 300  
 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly  
 305 310 315  
 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln  
 320 325 330  
 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp  
 335 340 345  
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu  
 350 355 360  
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln  
 365 370 375  
 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu  
 380 385 390  
 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala  
 395 400 405  
 Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu  
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 Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu Gln Leu Asp Tyr  
 425 430 435  
 Lys Asp Asp Asp Asp Lys  
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<210> 10  
 <211> 658  
 <212> PRT  
 <213> Artificial sequence

<220>  
 <223> hSu(fu)-GST protein

<400> 10  
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Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu



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His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys  
35 40 45

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp  
50 55 60

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile  
65 70 75

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala  
80 85 90

Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly  
95 100 105

Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val  
110 115 120

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp  
125 130 135

Arg Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His  
140 145 150

Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met  
155 160 165

Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys  
170 175 180

Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser  
185 190 195

Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe  
200 205 210

Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg Gly  
215 220 225

Ser Ala Glu Leu Arg Pro Ser Gly Ala Pro Gly Pro Thr Ala Pro  
230 235 240

Pro Ala Pro Gly Pro Thr Ala Pro Pro Ala Phe Ala Ser Leu Phe  
245 250 255

Pro Pro Gly Leu His Ala Ile Tyr Gly Glu Cys Arg Arg Leu Tyr  
260 265 270

Pro Asp Gln Pro Asn Pro Leu Gln Val Thr Ala Ile Val Lys Tyr  
275 280 285

Trp Leu Gly Gly Pro Asp Pro Leu Asp Tyr Val Ser Met Tyr Arg  
290 295 300

Asn Val Gly Ser Pro Ser Ala Asn Ile Pro Glu His Trp His Tyr  
305 310 315

Ile Ser Phe Gly Leu Ser Asp Leu Tyr Gly Asp Asn Arg Val His  
320 325 330

Glu Phe Thr Gly Thr Asp Gly Pro Ser Gly Phe Gly Phe Glu Leu  
 335 340 345  
 Thr Phe Arg Leu Lys Arg Glu Thr Gly Glu Ser Ala Pro Pro Thr  
 350 355 360  
 Trp Pro Ala Glu Leu Met Gln Gly Leu Ala Arg Tyr Val Phe Gln  
 365 370 375  
 Ser Glu Asn Thr Phe Cys Ser Gly Asp His Val Ser Trp His Ser  
 380 385 390  
 Pro Leu Asp Asn Ser Glu Ser Arg Ile Gln His Met Leu Leu Thr  
 395 400 405  
 Glu Asp Pro Gln Met Gln Pro Val Gln Thr Pro Phe Gly Val Val  
 410 415 420  
 Thr Phe Leu Gln Ile Val Gly Val Cys Thr Glu Glu Leu His Ser  
 425 430 435  
 Ala Gln Gln Trp Asn Gly Gln Gly Ile Leu Glu Leu Leu Arg Thr  
 440 445 450  
 Val Pro Ile Ala Gly Gly Pro Trp Leu Ile Thr Asp Met Arg Arg  
 455 460 465  
 Gly Glu Thr Ile Phe Glu Ile Asp Pro His Leu Gln Glu Arg Val  
 470 475 480  
 Asp Lys Gly Ile Glu Thr Asp Gly Ser Asn Leu Ser Gly Val Ser  
 485 490 495  
 Ala Lys Cys Ala Trp Asp Asp Leu Ser Arg Pro Pro Glu Asp Asp  
 500 505 510  
 Glu Asp Ser Arg Ser Ile Cys Ile Gly Thr Gln Pro Arg Arg Leu  
 515 520 525  
 Ser Gly Lys Asp Thr Glu Gln Ile Arg Glu Thr Leu Arg Arg Gly  
 530 535 540  
 Leu Glu Ile Asn Ser Lys Pro Val Leu Pro Pro Ile Asn Pro Gln  
 545 550 555  
 Arg Gln Asn Gly Leu Ala His Asp Arg Ala Pro Ser Arg Lys Asp  
 560 565 570  
 Ser Leu Glu Ser Asp Ser Ser Thr Ala Ile Ile Pro His Glu Leu  
 575 580 585  
 Ile Arg Thr Arg Gln Leu Glu Ser Val His Leu Lys Phe Asn Gln  
 590 595 600  
 Glu Ser Gly Ala Leu Ile Pro Leu Cys Leu Arg Gly Arg Leu Leu  
 605 610 615  
 His Gly Arg His Phe Thr Tyr Lys Ser Ile Thr Gly Asp Met Ala  
 620 625 630

CKT  
a  
Sub B

Ile Thr Phe Val Ser Thr Gly Val Glu Gly Ala Phe Ala Thr Glu  
635 640 645  
Glu His Pro Tyr Ala Ala His Gly Pro Trp Leu Gln Leu  
650 655